SEQUENCE LISTING

<110> Guss, Bengt
Nilsson, Martin
Frykberg, Lars
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Lindberg, Martin

<120> Fibrinogen Binding Protein Originating from Coagulase-Negative Staphylococcus

<130> guss 09/147405

Sub I'

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<141> 1999-04-01

<150> PCT/SE97/10191
<151> 1997-06-18

<150> SE 9602496-3
<151> 1996-06-20

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<170> PatentIn Ver. 2.0

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1 5 10 15

gtg atc aat aat aat cag tca ata aac acc gac gat aat aac caa ata 95
Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile
20 25 30

att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca 143
Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser
35 40 45

gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca 191
Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr
50 55 60

ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag 239
Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu
65 70 75

gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act 287

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Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr
 80                  85                  90                  95

gcc caa caa cca tct cac aca aca ata aat aga gaa gaa tct gtt caa   335
Ala Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln
            100                 105                 110

aca agt gat aat gta gaa gat tca cac gta tca gat ttt gct aac tct   383
Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser
        115                 120                 125

aaa ata aaa gag agt aac act gaa tct ggt aaa gaa gag aat act ata   431
Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile
    130                 135                 140

gag caa cct aat aaa gta aaa gaa gat tca aca aca agt cag ccg tct   479
Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser
145                 150                 155

ggc tat aca aat ata gat gaa aaa att tca aat caa gat gag tta tta   527
Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu
160                 165                 170                 175

aat tta cca ata aat gaa tat gaa aat aag gct aga cca tta tct aca   575
Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr
            180                 185                 190

aca tct gcc caa cca tcg att aaa cgt gta acc gta aat caa tta gcg   623
Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala
        195                 200                 205

gcg gaa caa ggt tcg aat gtt aac cat tta att aaa gtt act gat caa   671
Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln
    210                 215                 220

agt att act gaa gga tat gat gat agt gaa ggt gtt att aaa gca cat   719
Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His
225                 230                 235

gat gct gaa aac tta atc tat gat gta act ttt gaa gta gat gat aag   767
Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys
240                 245                 250                 255

gtg aaa tct ggt gat acg atg aca gtg gat ata gat aag aat aca gtt   815
Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val
            260                 265                 270

cca tca gat tta acc gat agc ttt aca ata cca aaa ata aaa gat aat   863
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Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn
          275                 280                 285

tct gga gaa atc atc gct aca ggt act tat gat aac aaa aat aaa caa   911
Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln
        290                 295                 300

atc acc tat act ttt aca gat tat gta gat aag tat gaa aat att aaa   959
Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys
    305                 310                 315

gca cac ctt aaa tta acg tca tac att gat aaa tca aag gtt cca aat   1007
Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn
320                 325                 330                 335

aat aat acc aag tta gat gta gaa tat aaa acg gcc ctt tca tca gta   1055
Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val
                340                 345                 350

aat aaa aca att acg gtt gaa tat caa aga cct aac gaa aat cgg act   1103
Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr
            355                 360                 365

gct aac ctt caa agt atg ttt aca aat ata gat acg aaa aat cat aca   1151
Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr
        370                 375                 380

gtt gag caa acg att tat att aac cct ctt cgt tat tca gcc aag gaa   1199
Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu
    385                 390                 395

aca aat gta aat att tca ggg aat ggt gat gaa ggt tca aca att ata   1247
Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile
400                 405                 410                 415

gac gat agc aca ata att aaa gtt tat aag gtt gga gat aat caa aat   1295
Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn
                420                 425                 430

tta cca gat agt aac aga att tat gat tac agt gaa tat gaa gat gtc   1343
Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val
            435                 440                 445

aca aat gat gat tat gcc caa tta gga aat aat aat gat gtg aat att   1391
Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile
        450                 455                 460

aat ttt ggt aat ata gat tca cca tat att att aaa gtt att agt aaa   1439
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Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys
465                 470                 475

tat gac cct aat aag gat gat tac acg act ata cag caa act gtg aca   1487
Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr
480                 485                 490                 495

atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc   1535
Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser
                500                 505                 510

tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt   1583
Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly
            515                 520                 525

gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa   1631
Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu
        530                 535                 540

gat gta gat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg   1679
Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro
    545                 550                 555

ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa   1727
Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys
560                 565                 570                 575

tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag   1775
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<211> 593
<212> PRT
<213> Staphylococcus epidermidis

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             20                  25                  30

Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu
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35 40 45

Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe
50 55 60

Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val
65 70 75 80

Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala
85 90 95

Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr
100 105 110

Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys
115 120 125

Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu
130 135 140

Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly
145 150 155 160

Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn
165 170 175

Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr
180 185 190

Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala
195 200 205

Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser
210 215 220

Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp
225 230 235 240

Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val
245 250 255

Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro
260 265 270

Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser
275 280 285

Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile

290 295 300

Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala
305 310 315 320

His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn
325 330 335

Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn
340 345 350

Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr Ala
355 360 365

Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr Val
370 375 380

Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr
385 390 395 400

Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp
405 410 415

Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu
420 425 430

Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr
435 440 445

Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile Asn
450 455 460

Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr
465 470 475 480

Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr Met
485 490 495

Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr
500 505 510

Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp
515 520 525

Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp
530 535 540

Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu

545 550 555 560

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gaagatagaa cagagtcaac aacaaatgta gatgaaaacg aagcaacatt tttacaaaag 180

acccctcaag ataatactca tcttacagaa gaagaggtaa aagaatcctc atcagtcgaa 240

tcctcaaatt catcaattga tactgcccaa caaccatctc acacaacaat aaatagagaa 300

gaatctgttc aaacaagtga taatgtagaa gattcacacg tatcagattt tgctaactct 360

aaaataaaag agagtaacac tgaatctggt aaagaagaga atactataga gcaacctaat 420

aaagtaaaag aagattcaac aacaagtcag ccgtctggct atacaaatat agatgaaaaa 480

atttcaaatc aagatgagtt attaaattta ccaataaatg aatatgaaaa taaggctaga 540

ccattatcta caacatctgc ccaaccatcg attaaacgtg taaccgtaaa tcaattagcg 600

gcggaacaag gttcgaatgt taaccattta attaaagtta ctgatcaaag tattactgaa 660

ggatatgatg atagtgaagg tgttattaaa gcacatgatg ctgaaaactt aatctatgat 720

gtaacttttg aagtagatga taaggtgaaa tctggtgata cgatgacagt ggatatagat 780

aagaatacag ttccatcaga tttaaccgat agctttacaa taccaaaaat aaaagataat 840

tctggagaaa tcatcgctac aggtacttat gataacaaaa ataaacaaat cacctatact 900

tttacagatt atgtagataa gtatgaaaat attaaagcac accttaaatt aacgtcatac 960

attgataaat caaaggttcc aaataataat accaagttag atgtagaata taaaacggcc 1020

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gctaaccttc aaagtatgtt tacaaatata gatacgaaaa atcatacagt tgagcaaacg 1140

atttatatta accctcttcg ttattcagcc aaggaaacaa atgtaaatat ttcagggaat 1200

ggtgatgaag gttcaacaat tatagacgat agcacaataa ttaaagttta taaggttgga 1260

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acgactatac agcaaactgt gacaatgcag acgactataa atgagtatac tggtgagttt 1500

agaacagcat cctatgataa tacaattgct ttctctacaa gttcaggtca aggacaaggt 1560

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gatggtattc aaaatacaaa tgataatgaa aaaccgctta gtaatgtatt ggtaactttg 1680

acgtatcctg atggaacttc aaaatcagtc agaacagatg aagatgggaa atatcaattt 1740

gatg 1744

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Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr
35 40 45

Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp
50 55 60

Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser Ser Val Glu
65 70 75 80

Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser His Thr Thr
85 90 95

Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val Glu Asp Ser
100 105 110

His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu
115 120 125

Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Lys Glu
130 135 140

Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys
145 150 155 160

Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr Glu
165 170 175

Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ile Lys
180 185 190

Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val Asn
195 200 205

His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp
210 215 220

Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr Asp
225 230 235 240

Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met Thr
245 250 255

Val Asp Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser Phe
260 265 270

Thr Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly
275 280 285

Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr
290 295 300

Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser Tyr
305 310 315 320

Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val Glu
325 330 335

Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu Tyr
340 345 350

Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe Thr
355 360 365

Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile Asn
370 375 380

Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly Asn
385 390 395 400

Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys Val
405 410 415

Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr
420 425 430

Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu
435 440 445

Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro
450 455 460

Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr
465 470 475 480

Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu Tyr
485 490 495

Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser
500 505 510

Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr
515 520 525

Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile Gln
530 535 540

Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr Leu
545 550 555 560

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565 570 575

Lys Tyr Gln Phe Asp
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tta cta act aaa aag aaa cct ata gca aat aaa tcc aat aaa tat gca 101
Leu Leu Thr Lys Lys Lys Pro Ile Ala Asn Lys Ser Asn Lys Tyr Ala
10 15 20

att aga aaa ttc aca gta ggt aca gcg tct att gta ata ggt gca aca 149
Ile Arg Lys Phe Thr Val Gly Thr Ala Ser Ile Val Ile Gly Ala Thr
25 30 35

tta ttg ttt ggt tta ggt cat aat gag gcc aaa gcc gag gag aat tca 197
Leu Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Ser
40 45 50 55

gta caa gac gtt aaa gat tcg aat acg gat gat gaa tta tca gac agc 245
Val Gln Asp Val Lys Asp Ser Asn Thr Asp Asp Glu Leu Ser Asp Ser
60 65 70

aat gat cag tct agt gat gaa gaa aag aat gat gtg atc aat aat aat 293
Asn Asp Gln Ser Ser Asp Glu Glu Lys Asn Asp Val Ile Asn Asn Asn
75 80 85

cag tca ata aac acc gac gat aat aac caa ata att aaa aaa gaa gaa 341
Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile Lys Lys Glu Glu
90 95 100

acg aat aac tac gat ggc ata gaa aaa cgc tca gaa gat aga aca gag 389
Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu Asp Arg Thr Glu
105 110 115

tca aca aca aat gta gat gaa aac gaa gca aca ttt tta caa aag acc 437

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Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr
120                 125                 130                 135

cct caa gat aat act cat ctt aca gaa gaa gag gta aaa gaa tcc tca   485
Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val Lys Glu Ser Ser
                140                 145                 150

tca gtc gaa tcc tca aat tca tca att gat act gcc caa caa cca tct   533
Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala Gln Gln Pro Ser
            155                 160                 165

cac aca aca ata aat aga gaa gaa tct gtt caa aca agt gat aat gta   581
His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr Ser Asp Asn Val
        170                 175                 180

gaa gat tca cac gta tca gat ttt gct aac tct aaa ata aaa gag agt   629
Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys Ile Lys Glu Ser
    185                 190                 195

aac act gaa tct ggt aaa gaa gag aat act ata gag caa cct aat aaa   677
Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys
200                 205                 210                 215

gta aaa gaa gat tca aca aca agt cag ccg tct ggc tat aca aat ata   725
Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly Tyr Thr Asn Ile
                220                 225                 230

gat gaa aaa att tca aat caa gat gag tta tta aat tta cca ata aat   773
Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn
            235                 240                 245

gaa tat gaa aat aag gct aga cca tta tct aca aca tct gcc caa cca   821
Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro
        250                 255                 260

tcg att aaa cgt gta acc gta aat caa tta gcg gcg gaa caa ggt tcg   869
Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser
    265                 270                 275

aat gtt aac cat tta att aaa gtt act gat caa agt att act gaa gga   917
Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly
280                 285                 290                 295

tat gat gat agt gaa ggt gtt att aaa gca cat gat gct gaa aac tta   965
Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp Ala Glu Asn Leu
                300                 305                 310

atc tat gat gta act ttt gaa gta gat gat aag gtg aaa tct ggt gat  1013
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Sub I)

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Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp
            315                 320                 325

acg atg aca gtg gat ata gat aag aat aca gtt cca tca gat tta acc   1061
Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr
        330                 335                 340

gat agc ttt aca ata cca aaa ata aaa gat aat tct gga gaa atc atc   1109
Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile
    345                 350                 355

gct aca ggt act tat gat aac aaa aat aaa caa atc acc tat act ttt   1157
Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln Ile Thr Tyr Thr Phe
360                 365                 370                 375

aca gat tat gta gat aag tat gaa aat att aaa gca cac ctt aaa tta   1205
Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu
                380                 385                 390

acg tca tac att gat aaa tca aag gtt cca aat aat aat acc aag tta   1253
Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu
            395                 400                 405

gat gta gaa tat aaa acg gcc ctt tca tca gta aat aaa aca att acg   1301
Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr
        410                 415                 420

gtt gaa tat caa aga cct aac gaa aat cgg act gct aac ctt caa agt   1349
Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser
    425                 430                 435

atg ttt aca aat ata gat acg aaa aat cat aca gtt gag caa acg att   1397
Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile
440                 445                 450                 455

tat att aac cct ctt cgt tat tca gcc aag gaa aca aat gta aat att   1445
Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile
                460                 465                 470

tca ggg aat ggt gat gaa ggt tca aca att ata gac gat agc aca ata   1493
Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile
            475                 480                 485

att aaa gtt tat aag gtt gga gat aat caa aat tta cca gat agt aac   1541
Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn
        490                 495                 500

aga att tat gat tac agt gaa tat gaa gat gtc aca aat gat gat tat   1589
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SUB I'

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Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr
    505                 510                 515

gcc caa tta gga aat aat aat gat gtg aat att aat ttt ggt aat ata   1637
Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile
520                 525                 530                 535

gat tca cca tat att att aaa gtt att agt aaa tat gac cct aat aag   1685
Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys
            540                 545                 550

gat gat tac acg act ata cag caa act gtg aca atg cag acg act ata   1733
Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile
        555                 560                 565

aat gag tat act ggt gag ttt aga aca gca tcc tat gat aat aca att   1781
Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile
    570                 575                 580

gct ttc tct aca agt tca ggt caa gga caa ggt gac ttg cct cct gaa   1829
Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu
585                 590                 595

aaa act tat aaa atc gga gat tac gta tgg gaa gat gta gat aaa gat   1877
Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp
600                 605                 610                 615

ggt att caa aat aca aat gat aat gaa aaa ccg ctt agt aat gta ttg   1925
Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu
            620                 625                 630

gta act ttg acg tat cct gat gga act tca aaa tca gtc aga aca gat   1973
Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp
        635                 640                 645

gaa gat ggg aaa tat caa ttt gat gga ttg aaa aac gga ttg act tat   2021
Glu Asp Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn Gly Leu Thr Tyr
    650                 655                 660

aaa att aca ttc gaa aca cct gaa gga tat acg ccg acg ctt aaa cat   2069
Lys Ile Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His
665                 670                 675

tca gga aca aat cct gca cta gac tca gaa ggt aat tct gta tgg gta   2117
Ser Gly Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val
680                 685                 690                 695

act att aat gga caa gac gat atg acg att gat agt gga ttt tat caa   2165
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Thr Ile Asn Gly Gln Asp Asp Met Thr Ile Asp Ser Gly Phe Tyr Gln
                700                 705                 710

aca cct aaa tac agc tta ggg aac tat gta tgg tat gac act aat aaa   2213
Thr Pro Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr Asp Thr Asn Lys
            715                 720                 725

gat ggt att caa ggt gat gat gaa aaa gga atc tct gga gtt aaa gtg   2261
Asp Gly Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val
        730                 735                 740

acg tta aaa gat gaa aac gga aat atc att agt aca act aca acc gat   2309
Thr Leu Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Thr Asp
    745                 750                 755

gaa aat gga aag tat caa ttt gat aat tta aat agt ggt aat tat att   2357
Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile
760                 765                 770                 775

gtt cat ttt gat aaa cct tca ggt atg act caa aca aca aca gat tct   2405
Val His Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Thr Asp Ser
                780                 785                 790

ggt gat gat gac gaa cag gat gct gat ggg gaa gaa gtt cat gta aca   2453
Gly Asp Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr
            795                 800                 805

att act gat cat gat gac ttt agt ata gat aac gga tac tat gat gac   2501
Ile Thr Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp
        810                 815                 820

gaa tcg gat tcc gat agt gac tca gac agc gac tca gat tcc gat agt   2549
Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
    825                 830                 835

gat tca gac tcc gat agc gac tcg gat tca gac agc gac tca gat tca   2597
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
840                 845                 850                 855

gac agc gac tcg gat tct gat agc gac tcg gat tca gac agc gac tca   2645
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
                860                 865                 870

gac tca gac agt gat tca gat tca gac agc gac tca gat tcc gat agt   2693
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
            875                 880                 885

gat tca gac tca gac agc gac tca gat tct gat agt gat tca gac tca   2741
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Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
        890                 895                 900

gac agt gat tca gat tca gac agc gac tca gat tcc gat agt gat tca   2789
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
    905                 910                 915

gac tca gac agc gac tca gat tcc gat agt gat tca gac tca gac agc   2837
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
920                 925                 930                 935

gac tca gat tct gat agt gat tca gac tca gac agt gat tca gac tca   2885
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
                940                 945                 950

gac agt gat tca gat tcc gat agt gat tca gac tcc gat agc gac tca   2933
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
            955                 960                 965

gac tcg gat agt gac tca gat tct gat agt gat tca gac tcc gat agc   2981
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
        970                 975                 980

gac tca gac tcg gat agt gac tca gat tct gat agt gat tca gac tca   3029
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
    985                 990                 995

gac agc gac tca gat tct gat agt gat tca gac tca gtc agt gat tca   3077
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Val Ser Asp Ser
1000                1005                1010                1015

gat tcc gat agt gat tca gac tca ggc agt gat tcg gat tcc gat agt   3125
Asp Ser Asp Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp Ser Asp Ser
                1020                1025                1030

gat tca gac tca gac aac gac tca gat tta ggc aat agc tca gat aag   3173
Asp Ser Asp Ser Asp Asn Asp Ser Asp Leu Gly Asn Ser Ser Asp Lys
            1035                1040                1045

agt aca aaa gat aaa tta cct gat aca gga gct aat gaa gat tat ggc   3221
Ser Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp Tyr Gly
        1050                1055                1060

tct aaa ggc acg tta ctt gga act ctg ttt gca ggt tta gga gcg tta   3269
Ser Lys Gly Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala Leu
    1065                1070                1075

tta tta ggg aaa cgt cgc aaa aat aga aaa aat aaa aat taaaatgttc   3318
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```
Leu Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn
1080                1085                1090

aaatgaaatt tgtagaaaga agcagatatg agatttgaat agaaagtaga tttagtccaa 3378

caaatgtaag atgttgatta aaactataat ataactttca cgtttatcat atcttgtgaa 3438

aaagatgatg caaacaaggt catttctatt aaaaatgact taaatgtatg atttttagag 3498

aaacatatac aactcacaat ctgacaatga tttaatagag gaaccgtgaa ttttaaatga 3558

attcatggtt ccttttttatt gaattaataa aaattctttt at                    3600
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Sub I'

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<211> 1092
<212> PRT
<213> Staphylococcus epidermidis

<400> 15
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  1               5                  10                  15

Asn Lys Ser Asn Lys Tyr Ala Ile Arg Lys Phe Thr Val Gly Thr Ala
             20                  25                  30

Ser Ile Val Ile Gly Ala Thr Leu Leu Phe Gly Leu Gly His Asn Glu
         35                  40                  45

Ala Lys Ala Glu Glu Asn Ser Val Gln Asp Val Lys Asp Ser Asn Thr
     50                  55                  60

Asp Asp Glu Leu Ser Asp Ser Asn Asp Gln Ser Ser Asp Glu Glu Lys
 65                  70                  75                  80

Asn Asp Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn
                 85                  90                  95

Gln Ile Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys
            100                 105                 110

Arg Ser Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu
        115                 120                 125

Ala Thr Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu
    130                 135                 140

Glu Glu Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile
```

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145                 150                 155                 160

Asp Thr Ala Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser
                165                 170                 175

Val Gln Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala
            180                 185                 190

Asn Ser Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn
        195                 200                 205

Thr Ile Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln
    210                 215                 220

Pro Ser Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu
225                 230                 235                 240

Leu Leu Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu
                245                 250                 255

Ser Thr Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln
            260                 265                 270

Leu Ala Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr
        275                 280                 285

Asp Gln Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys
    290                 295                 300

Ala His Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp
305                 310                 315                 320

Asp Lys Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn
                325                 330                 335

Thr Val Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys
            340                 345                 350

Asp Asn Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn
        355                 360                 365

Lys Gln Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn
    370                 375                 380

Ile Lys Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val
385                 390                 395                 400

Pro Asn Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser
```

405 410 415

Ser Val Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn
420 425 430

Arg Thr Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn
435 440 445

His Thr Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala
450 455 460

Lys Glu Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr
465 470 475 480

Ile Ile Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn
485 490 495

Gln Asn Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu
500 505 510

Asp Val Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val
515 520 525

Asn Ile Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile
530 535 540

Ser Lys Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr
545 550 555 560

Val Thr Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr
565 570 575

Ala Ser Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly
580 585 590

Gln Gly Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val
595 600 605

Trp Glu Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu
610 615 620

Lys Pro Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr
625 630 635 640

Ser Lys Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly
645 650 655

Leu Lys Asn Gly Leu Thr Tyr Lys Ile Thr Phe Glu Thr Pro Glu Gly

660 665 670

Tyr Thr Pro Thr Leu Lys His Ser Gly Thr Asn Pro Ala Leu Asp Ser
675 680 685

Glu Gly Asn Ser Val Trp Val Thr Ile Asn Gly Gln Asp Asp Met Thr
690 695 700

Ile Asp Ser Gly Phe Tyr Gln Thr Pro Lys Tyr Ser Leu Gly Asn Tyr
705 710 715 720

Val Trp Tyr Asp Thr Asn Lys Asp Gly Ile Gln Gly Asp Asp Glu Lys
725 730 735

Gly Ile Ser Gly Val Lys Val Thr Leu Lys Asp Glu Asn Gly Asn Ile
740 745 750

Ile Ser Thr Thr Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Asp Asn
755 760 765

Leu Asn Ser Gly Asn Tyr Ile Val His Phe Asp Lys Pro Ser Gly Met
770 775 780

Thr Gln Thr Thr Thr Asp Ser Gly Asp Asp Asp Glu Gln Asp Ala Asp
785 790 795 800

Gly Glu Glu Val His Val Thr Ile Thr Asp His Asp Asp Phe Ser Ile
805 810 815

Asp Asn Gly Tyr Tyr Asp Asp Glu Ser Asp Ser Asp Ser Asp Ser Asp
820 825 830

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
835 840 845

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
850 855 860

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
865 870 875 880

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
885 890 895

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
900 905 910

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp

915 920 925

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
930 935 940

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
945 950 955 960

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
965 970 975

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
980 985 990

Sub I'>

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
995 1000 1005

Ser Asp Ser Val Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Gly
1010 1015 1020

C' cont

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Asn Asp Ser Asp
025 1030 1035 1040

Leu Gly Asn Ser Ser Asp Lys Ser Thr Lys Asp Lys Leu Pro Asp Thr
1045 1050 1055

Gly Ala Asn Glu Asp Tyr Gly Ser Lys Gly Thr Leu Leu Gly Thr Leu
1060 1065 1070

Phe Ala Gly Leu Gly Ala Leu Leu Leu Gly Lys Arg Arg Lys Asn Arg
1075 1080 1085

Lys Asn Lys Asn
1090